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20 25 30Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Val Ile Gly Thr
35 40 45Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys Leu Val
50 55 60Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser Pro Cys
65 70 75 80Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys Thr Lys
85 90 95Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp Pro Glu
100 105 110Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro
115 120 125Ser Gly Tyr Leu Gly Glu Asp Pro Arg Xaa Ile Pro Asn Asn Leu Met
130 135 140Pro Tyr Val Gln Gln Val Ala Val Gly Lys Xaa Pro Ala Leu Thr Val
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<213> Oryza sativa

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 aactcggctt ccgcgttgc gtcctcgaca acctcgacaa cgcctccgag ctcgcccattcc 240
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 <213> Oryza sativa

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 Val Leu Gln Leu Leu Gln Leu Gly Phe Arg Val Val Val Leu Asp Asn
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 Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu Arg Val Arg Glu Leu Ala
 35 40 45
 Gly His Asn Ala Asn Asn Leu Asp Phe Arg Lys Gly Asp Leu Arg Asp
 50 55 60
 Lys Gln Ala Leu Xaa Gln Ile Phe Ser Ser Gln Lys Val Glu Xaa Val
 65 70 75 80
 Ile Gln Phe Ala Gly Leu Lys Thr Val Gly Glu Xaa Val Lys Asn Pro
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 Xaa Phe Tyr

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<213> Glycine max

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tgggaccanc aacctctacg agtttatgg aaagtataat tgcaaaaaga tgggtttctc 420
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<210> 6
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<212> PRT
<213> Glycine max

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Ile Gly Thr His Thr Val Val Xaa Leu Leu Lys Ala Gly Phe Ser Val
20 25 30

Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Met Asp Arg
35 40 45

Val Arg Gln Val Val Gly Pro Leu Leu Ser Gln Asn Leu Gln Phe Thr
 50 55 60

Gln Gly Asp Leu Arg Asn Arg Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80

Thr Thr Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala
 85 90 95

Glu Ser Val Ala Lys Pro Arg Arg Tyr Phe Asp Phe Asn Leu Xaa Gly
 100 105 110

Thr Xaa Asn Leu Tyr Glu Phe Met Xaa Lys Tyr Asn Cys Lys Lys Met
 115 120 125

Gly Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Xaa Glu Lys Ile Pro
 130 135 140

Cys Glu Glu Asp
 145

<210> 7

<211> 520

<212> DNA

<213> *Triticum aestivum*

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<221> unsure

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<210> 8

<211> 162

<212> PRT

<213> *Triticum aestivum*

<400> 8
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Gln Leu Leu Glu Lys Gly Tyr Ala Val Thr Ala Val Asp Asn Phe His
 20 25 30

Asn Ser Val Pro Glu Ala Leu Asp Arg Val Arg His Ile Val Gly Pro
 35 40 45

Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp Leu Thr Ile Lys
 50 55 60

Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr Asp Ala Val Ile
 65 70 75 80

His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val Ala His Pro Glu
 85 90 95

Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn Leu Tyr Asp Val
 100 105 110

Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser Ser Ser Ala Thr
 115 120 125

Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu Asp Ser Pro Leu
 130 135 140

Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr Trp Arg Arg Ser
 145 150 155 160

Ala Arg

<210> 9
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 <213> Zea mays

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 ggataccgaa caacctgtcg ccctacatcc agcaggtcnc cgtcggnagg ctccccgagc 420
 tcaacgtcta cgggnacgta ttaccccacc cggggacggn accgcgtatca gggactacat 480
 acacgtcgtc gaactcgccg atgggcacat cgcaagggtc cangaactct ncgactctcc 540
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 <213> Zea mays

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 1 5 10 15

Ala His Pro Glu Met Tyr Tyr Glu Asn Asn Leu Ile Gly Thr Ile Asn
 20 25 30

Leu Tyr Lys Ser Met Lys Glu His Gly Cys Lys Lys Leu Val Phe Ser
 35 40 45

Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu
 50 55 60

Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 65 70 75 80

Leu Glu Asp Met Ala Arg Asp Tyr His Arg Ala Asp Thr Glu Trp Ser
 85 90 95

Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly
 100 105 110

Xaa Ile Xaa Arg Gly Pro Gln Gly Asp Thr Glu Gln Pro Ala Ala Leu
 115 120 125

His Pro Ala Gly Xaa Arg Arg Xaa Ala Pro Arg Ala Gln Arg Leu Arg
 130 135 140

Xaa Thr Ile Thr Pro Pro Gly Asp Gly Thr Ala Ile Arg Asp Tyr Ile
 145 150 155 160

His Val Val Glu Leu Ala Asp Gly His Ile Ala Arg Ala Xaa Glu Leu
 165 170 175

Xaa Asp Ser Pro Asp Ile Ser Cys Val Gly Tyr Asn Leu Gly Val Gln
 180 185 190

Gly Arg Arg Xaa Xaa
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<210> 11
 <211> 300
 <212> DNA
 <213> Oryza sativa

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<220>
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 acgaggacaa cgtcgccggc accatgaacc tctnctccgc cttgaccaag tacggcngcn 180
 agangatagt gttctcgctg tnggcgacng tgcgtncggcca gccgganaag accccctgctg 240
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<210> 12
 <211> 99
 <212> PRT
 <213> Oryza sativa

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<400> 12
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Tyr Asp Ala Val Ile His Phe Ala Gly Leu Lys Xaa Trp Gly Arg Ala
 20 25 30

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Ser Arg Asn Pro Gln Met Tyr Tyr Glu Asp Asn Val Ala Gly Thr Met
 35 40 45
 Asn Leu Xaa Ser Ala Leu Thr Lys Tyr Gly Xaa Xaa Xaa Ile Val Phe
 50 55 60
 Ser Ser Xaa Ala Thr Val Xaa Gly Gln Pro Xaa Lys Thr Pro Cys Val
 65 70 75 80
 Glu Xaa Ser Xaa Leu Ser Ala Leu Asn Pro Tyr Gly Ala Xaa Xaa Leu
 85 90 95
 Val Leu Glu

<210> 13
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 <212> DNA
 <213> Glycine max

<400> 13
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 gctggcttga aagcgggtgc tgaaagcgtt gcgaaggccc gtcgctattt tgatttaat 360
 ttgggtggca ccatcaacct ctacgagttt atggcaaaatg ataattgcaaa aaagatggtt 420
 ttctcatcat ctgcaaccgt ttatggccaa cctgaaaaga taccgtgtga ggaggatttc 480
 aagttacaag ctatgaatcc ctatggacgg accaagcttt tcttggaaaga aattggccga 540
 gatattcaga aagctgaacc agaatggaaatc atcatattac tgagatactt caatccagg 600
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<210> 14
 <211> 350
 <212> PRT
 <213> Glycine max

<400> 14
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 Ile Gly Thr His Thr Val Val Gln Leu Leu Lys Ala Gly Phe Ser Val
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 Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Val Asp Arg
 35 40 45

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Val	Arg	Gln	Val	Val	Gly	Pro	Leu	Leu	Ser	Gln	Asn	Leu	Gln	Phe	Thr
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Gln	Gly	Asp	Leu	Arg	Asn	Arg	Asp	Asp	Leu	Glu	Lys	Leu	Phe	Ser	Lys
65					70				75						80
Thr	Thr	Phe	Asp	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Ala
					85				90				95		
Glu	Ser	Val	Ala	Lys	Pro	Arg	Arg	Tyr	Phe	Asp	Phe	Asn	Leu	Val	Gly
					100				105			110			
Thr	Ile	Asn	Leu	Tyr	Glu	Phe	Met	Ala	Lys	Tyr	Asn	Cys	Lys	Lys	Met
					115			120			125				
Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Gln	Pro	Glu	Lys	Ile	Pro
						130		135			140				
Cys	Glu	Glu	Asp	Phe	Lys	Leu	Gln	Ala	Met	Asn	Pro	Tyr	Gly	Arg	Thr
					145			150			155			160	
Lys	Leu	Phe	Leu	Glu	Glu	Ile	Ala	Arg	Asp	Ile	Gln	Lys	Ala	Glu	Pro
					165				170			175			
Glu	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His
					180			185			190				
Glu	Ser	Gly	Lys	Leu	Gly	Glu	Asp	Pro	Lys	Gly	Ile	Pro	Asn	Asn	Leu
					195			200			205				
Met	Pro	Tyr	Ile	Gln	Gln	Val	Ala	Val	Gly	Arg	Leu	Thr	Glu	Leu	Asn
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Val	Tyr	Gly	His	Asp	Tyr	Pro	Thr	Arg	Asp	Gly	Ser	Ala	Ile	Arg	Asp
					225			230			235			240	
Tyr	Ile	His	Val	Met	Asp	Leu	Ala	Asp	Gly	His	Ile	Ala	Ala	Leu	Arg
					245			250			255				
Lys	Leu	Phe	Thr	Thr	Glu	Asn	Ile	Gly	Cys	Thr	Ala	Tyr	Asn	Leu	Gly
					260			265			270				
Thr	Gly	Arg	Gly	Thr	Ser	Val	Leu	Glu	Met	Val	Thr	Ala	Phe	Glu	Lys
					275			280			285				
Ala	Ser	Gly	Lys	Lys	Ile	Pro	Val	Lys	Leu	Cys	Pro	Arg	Arg	Pro	Gly
					290			295			300				
Asp	Ala	Thr	Glu	Val	Tyr	Ala	Ser	Thr	Glu	Arg	Ala	Glu	Lys	Leu	
					305			310			315			320	
Gly	Trp	Lys	Ala	Asn	Tyr	Gly	Val	Glu	Glu	Met	Cys	Arg	Asp	Gln	Trp
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Asn	Trp	Ala	Lys	Asn	Asn	Pro	Trp	Gly	Tyr	Ala	Gly	Lys	Pro		
					340			345			350				
<210> 15															
<211> 1516															

<212> DNA
 <213> *Triticum aestivum*

<220>
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 aaaaaaaaaa aaagaaaaaa aaaaagacaa aaaaaaaaaacg agaaaggaga aaaaaatgac 1380
 agaaggaaag agaaaaagaa ggccaaacgc ggggccccgc cgaacggacc gacggcgcgc 1440
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 gggcctcaa tccccg 1516

<210> 16
 <211> 352
 <212> PRT
 <213> *Triticum aestivum*

<400> 16
 Ala Arg Gly Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
 1 5 10 15

His Thr Val Leu Gln Leu Leu Glu Lys Gly Tyr Ala Val Thr Ala Val
 20 25 30

Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Asp Arg Val Arg His
 35 40 45

Ile Val Gly Pro Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp
 50 55 60

Leu Thr Ile Lys Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr
 65 70 75 80

Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val
 85 90 95

Ala His Pro Glu Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn
 100 105 110
 Leu Tyr Asp Val Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser
 115 120 125
 Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu
 130 135 140
 Asp Ser Pro Leu Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr
 145 150 155 160
 Leu Glu Glu Met Leu Arg Asp Tyr Gln His Ala Asn Pro Glu Trp Arg
 165 170 175
 Thr Ile Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Glu Ser Gly
 180 185 190
 Asp Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr
 195 200 205
 Ile Gln Gln Val Ala Val Ala Arg Arg Pro Glu Leu Asn Val Tyr Gly
 210 215 220
 His Asp Tyr Arg Thr Arg Asp Gly Thr Ala Val Arg Asp Tyr Ile His
 225 230 235 240
 Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Glu Lys Leu Phe
 245 250 255
 Ala Thr Pro Asp Ile Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg
 260 265 270
 Gly Thr Thr Val Leu Glu Met Val Ser Ala Phe Glu Lys Ala Tyr Gly
 275 280 285
 Lys Lys Ile Pro Val Lys Met Cys Pro Arg Arg Pro Gly Asp Ser Glu
 290 295 300
 Gln Val Tyr Ala Ser Thr Ala Lys Ala Glu Glu Glu Leu Gly Trp Arg
 305 310 315 320
 Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala
 325 330 335
 Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Asn Ala Ala Glu Asn Lys Asp
 340 345 350
 <210> 17
 <211> 1393
 <212> DNA
 <213> Zea mays
 <400> 17
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 tactttatta tgacaacaac gtcattggca cgataaatct tctagaagtt atgtctgttc 180
 acgggtgcaa gaagttggtg ttctcatcat cagctgcagt ttatggatca cccaaaaact 240
 caccctgcac agaaaatttt cctcttactc caaacaatcc atatggcaaa acaaagctcg 300
 ttgttgaaga tatttgcgg gatatctacc gttcagatcc tgaatggaag atcattttac 360

ttaggtactt	caatccagg	ttgtgtcatc	ctagtggata	tcttggcgag	gacccacgag	420
gaattccaa	caatctttag	ccctatgttc	agcaagttgc	ggttggtagg	aggccagctc	480
taacagttt	aggaaatgac	tatgcaacaa	gagatggac	tggggtccga	gattacatcc	540
atgtgggt	ccttgctgac	ggacatattg	ctgcattgca	gaagctttt	gagaactcta	600
gcatagggt	tgaagcgtac	aaccctggaa	ccggaagagg	tacatctgtg	ctggagattg	660
ttaaagcatt	tgagaaggct	tctgggaaga	aaataccct	gatttttgtt	gaaagacgcc	720
caggtgatgc	agagattctg	ttttcagaga	ctactaaagc	agagagggag	cttaactgga	780
aagcaaaata	cggatttggaa	gagatgtgcc	gcccccaatg	gaactgggc	agcaagaacc	840
cttatggcta	tggatcacct	gactctatca	agcagaatgg	tcaccaaaca	aacggatccg	900
ctgactcctc	caaggcagaat	ggccaccgca	caaacggtt	aactgactca	cccaagcgg	960
acggccacca	tgcgtatggg	tctgctgact	cacccaaagcg	caacgggcac	tgcgtttttg	1020
gatcatcaga	cctcaagccg	aatggtaatg	gccacctgcg	ctgagcagaa	ctgtttggcc	1080
tgtgagctcc	ctgtacattc	ggttgcgtat	tgagctccct	gcacgttcgg	tcgaggtcta	1140
tcgtgaacccc	actatccgag	attgatgtgg	atcattgggt	tgacaggtca	tacagtatag	1200
agccggtggc	agaggaattc	ctgtttgctg	tgggtaaagc	tatcttctg	cttcgtgtt	1260
ttttcttgct	tctttcgatt	atggttagg	aatgtgtca	taatgttata	gctgattatc	1320
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aaaaaaaaaa	aaa					1393

<210> 18

<211> 353

<212> PRT

<213> Zea mays

<400> 18

Thr	Arg	Ile	Asp	Leu	Arg	Asp	Lys	Gly	Ala	Leu	Glu	Met	Val	Phe	Ala
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Ser	Thr	Arg	Phe	Glu	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val
						20			25			30			

Gly	Glu	Ser	Val	Gln	Lys	Pro	Leu	Leu	Tyr	Tyr	Asp	Asn	Asn	Val	Ile
							35		40			45			

Gly	Thr	Ile	Asn	Leu	Leu	Glu	Val	Met	Ser	Val	His	Gly	Cys	Lys	Lys
						50		55			60				

Leu	Val	Phe	Ser	Ser	Ser	Ala	Ala	Val	Tyr	Gly	Ser	Pro	Lys	Asn	Ser
65							70			75			80		

Pro	Cys	Thr	Glu	Asn	Phe	Pro	Leu	Thr	Pro	Asn	Asn	Pro	Tyr	Gly	Lys
					85			90					95		

Thr	Lys	Leu	Val	Val	Glu	Asp	Ile	Cys	Arg	Asp	Ile	Tyr	Arg	Ser	Asp
					100			105			110				

Pro	Glu	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala
					115			120			125				

His	Pro	Ser	Gly	Tyr	Leu	Gly	Glu	Asp	Pro	Arg	Gly	Ile	Pro	Asn	Asn
					130			135			140				

Leu	Met	Pro	Tyr	Val	Gln	Gln	Val	Ala	Val	Gly	Arg	Arg	Pro	Ala	Leu
					145			150		155				160	

Thr	Val	Leu	Gly	Asn	Asp	Tyr	Ala	Thr	Arg	Asp	Gly	Thr	Gly	Val	Arg
					165			170			175				

Asp	Tyr	Ile	His	Val	Val	Asp	Leu	Ala	Asp	Gly	His	Ile	Ala	Ala	Leu
					180			185			190				

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Gln Lys Leu Phe Glu Asn Ser Ser Ile Gly Cys Glu Ala Tyr Asn Leu
 195 200 205
 Gly Thr Gly Arg Gly Thr Ser Val Leu Glu Ile Val Lys Ala Phe Glu
 210 215 220
 Lys Ala Ser Gly Lys Lys Ile Pro Leu Ile Phe Gly Glu Arg Arg Pro
 225 230 235 240
 Gly Asp Ala Glu Ile Leu Phe Ser Glu Thr Thr Lys Ala Glu Arg Glu
 245 250 255
 Leu Asn Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln
 260 265 270
 Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
 275 280 285
 Ile Lys Gln Asn Gly His Gln Thr Asn Gly Ser Ala Asp Ser Ser Lys
 290 295 300
 Gln Asn Gly His Arg Thr Asn Gly Ser Thr Asp Ser Pro Lys Arg Asn
 305 310 315 320
 Gly His His Ala Tyr Gly Ser Ala Asp Ser Pro Lys Arg Asn Gly His
 325 330 335
 Cys Val Phe Gly Ser Ser Asp Leu Lys Pro Asn Gly Asn Gly His Leu
 340 345 350

Arg

<210> 19
 <211> 1498
 <212> DNA
 <213> Oryza sativa

<400> 19
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 cacacacgca cacaacaaca acaagatcaa tcaaagtata agaagatggg ttcggccttg 120
 ttgcggacga tcctggtgac gggcgccgccc ggctacatcg gcagccacac cgtccctccag 180
 cttctccaac tcggcttccg cggtgtcgct ctcgacaacc tcgacaacgc ctccgagctc 240
 gccatctcc gcgtcaggga actcgccgga cacaacgcca acaacctcga ctccgcaag 300
 gttgacctcc gcgacaagca agcgttggac caaatcttct cctctcaaaag gtttggggct 360
 gtcatccatt ttgcgggct gaaagctgtt ggcgagagcg tgcaagaagcc cctgcattac 420
 tacgacaaca acctcatcg caccatact ctcctgcagg tcatggccgc acatggctgc 480
 accaaagctgg tggctcatac atccgcaact gtctacgggt gggccaaagg ggtgccctgc 540
 actgaagaat ccccactttg tgcaatgaac ccctacggca gaacaaagct ggtaatcgaa 600
 gacatgtgcc gggatctgca tgcctcagac ccaaactgga agatcatact gctccgatac 660
 ttcaaccctg ttggagctca cccaaagcggg tacattggtg aggacccctg cggcatccca 720
 aacaacctca tgccttcgt ccagcaggc gctgttggca ggaggccggc ctttaccgtc 780
 tatggAACCG actacaacac caaggatgga actggggttc gtgactataat ccatgttgg 840
 gatctagcgg atggcatat cggccgtta aggaagctct atgaagattc tgatagaata 900
 gggatgtgagg tggataatct gggactgga aaggggacat ctgtgtggaa aatggttgca 960
 gcattcgaga aagcttctgg aaagaaaatc ccgttggat ttgctggacg aaggcctgga 1020
 gatgccgaga tcgttacgc tcaaactgccc aaagctgaga aggaactgaa atggaaaggca 1080
 aaatacgggg tagaggagat gtgcaggac ctgtggaaatt gggcgagcaa gaaccctac 1140
 gggtatggat cgccggacag tagcaactga tccagctgaa tataggcgtc caatcccca 1200

gtagcagcag cagcagcatg acttctatac atatatataat ataatacataa agaatgaaga 1260
 aacaaagaat tcggacttgt tgagttacta ctactactac tactaatccc atctgatgga 1320
 ccgcattgtt tagggggcctt gttaggggtcc agcagcttca tcatacgtct ccttaggagg 1380
 cctctaataat aatctccata tttatggtag aaataaaattt tgcccaccgt ggaagaacta 1440
 tataatagaa tcatacgtat ttgttgatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1498

<210> 20
 <211> 354
 <212> PRT
 <213> Oryza sativa

<400> 20
 Met Val Ser Ala Leu Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly
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 Tyr Ile Gly Ser His Thr Val Leu Gln Leu Leu Gln Leu Gly Phe Arg
 20 25 30
 Val Val Val Leu Asp Asn Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu
 35 40 45
 Arg Val Arg Glu Leu Ala Gly His Asn Ala Asn Asn Leu Asp Phe Arg
 50 55 60
 Lys Val Asp Leu Arg Asp Lys Gln Ala Leu Asp Gln Ile Phe Ser Ser
 65 70 75 80
 Gln Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
 85 90 95
 Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly
 100 105 110
 Thr Ile Thr Leu Leu Gln Val Met Ala Ala His Gly Cys Thr Lys Leu
 115 120 125
 Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro
 130 135 140
 Cys Thr Glu Glu Ser Pro Leu Cys Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160
 Lys Leu Val Ile Glu Asp Met Cys Arg Asp Leu His Ala Ser Asp Pro
 165 170 175
 Asn Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190
 Pro Ser Gly Tyr Ile Gly Glu Asp Pro Cys Gly Ile Pro Asn Asn Leu
 195 200 205
 Met Pro Phe Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr
 210 215 220
 Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp
 225 230 235 240
 Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255

Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu
 260 265 270

Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu
 275 280 285

Lys Ala Ser Gly Lys Ile Pro Leu Val Phe Ala Gly Arg Arg Pro
 290 295 300

Gly Asp Ala Glu Ile Val Tyr Ala Gln Thr Ala Lys Ala Glu Lys Glu
 305 310 315 320

Leu Lys Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Leu
 325 330 335

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
 340 345 350

Ser Asn

<210> 21

<211> 1532

<212> DNA

<213> Glycine max

<400> 21

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 tccccctact ttcgctcacc acttaagatt tccacaacaacc cctctctgca aaacgcttcg 180
 cataaggtac ttatgcgcga taagactgtt ctggtaaccg gcccggccgg ttacatcgcc 240
 agccacaccg ttcttcagct cttgctcgga gtttcagag ccgtcgctct cgacaacctc 300
 gaaaattcct ccgagggttgc catccacaga gtcaggagtc tcgccccggcga atttggAAC 360
 aacctctcct ttcacacaaggt ggacctacgg gacagagctg ctctagacca aatattttct 420
 tccacacaat tcgatgttgtt catabatttt gctggactga aagcagttagg agaaagtgtg 480
 caaaaacctt tactatacta taacaacaac ttgactggc caatcactct attggaaagtc 540
 atggctgccc atggatgcaaa gaagctcggt ttttcatctt cagcaactgt atatggttgg 600
 ccaaaggagg ttccatgcac agaagagtcc cctctgtcag caatgaaccc atatgacga 660
 actaagctt tcattgaaga aatttgcgt gatgtccact gtgcagagcc agattgtaaa 720
 ataattttgt taagatactt caaccccgat ggtgcacacc ccagtggta tattggggag 780
 gatccctgtg gaattccaaa caatctcatg ccatttggc agcaagttagc agttggccga 840
 cggcctgcac tgacagttt tggaaatgat tataatacaa gtgatggcact tgggggttgg 900
 gattacattc atgttgtga ttttagcagat gggcacattt ctgcattgtct taaactagat 960
 gaacctataa taggttgtga ggtttataac ctgggaacag gaaaggAAC atcagttttg 1020
 gagatggta gagctttga aatggcatct ggaaagaaaa ttccacttgt gatggctggc 1080
 cgtagacctg gtgatgtca aattgtttat gcatcaacaa agaaagcgga aagagagctt 1140
 aaatggaaagg caaaatatgg cattgatgag atgtgcgtg atcaatggaa ttgggttagc 1200
 aaaaaccctt atggctatgg agatcaggc tccaccgatt aaccacttag ttttctcttt 1260
 gggttctttt ctgaactcac ccacaccgtt gtccgttaggt ctgtgaatt tagttttccc 1320
 aaaagctttt ctttcttttag tgatcttaag gtgacaaagt acttgtatttta ttactattca 1380
 tagttacata gtaagtaagt agtggtttac tatactgtaa tttaaagggtt ctcttaggttc 1440
 cttcttacag gttattgttattttagtcc gattctctca tggccacat gagcagcatc 1500
 ctgtttgtta aatctaaatc acatgtttgtt tt 1532

<210> 22

<211> 349

<212> PRT

<213> Glycine max

<400> 22
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 Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Arg Ala Val Val
 20 25 30
 Leu Asp Asn Leu Glu Asn Ser Ser Glu Val Ala Ile His Arg Val Arg
 35 40 45
 Glu Leu Ala Gly Glu Phe Gly Asn Asn Leu Ser Phe His Lys Val Asp
 50 55 60
 Leu Arg Asp Arg Ala Ala Leu Asp Gln Ile Phe Ser Ser Thr Gln Phe
 65 70 75 80
 Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
 85 90 95
 Gln Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Thr Gly Thr Ile Thr
 100 105 110
 Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
 115 120 125
 Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu
 130 135 140
 Glu Phe Pro Leu Ser Ala Met Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 145 150 155 160
 Ile Glu Glu Ile Cys Arg Asp Val His Cys Ala Glu Pro Asp Cys Lys
 165 170 175
 Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
 180 185 190
 Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
 195 200 205
 Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
 210 215 220
 Asn Asp Tyr Asn Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
 225 230 235 240
 Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Leu Lys Leu Asp
 245 250 255
 Glu Pro Asn Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
 260 265 270
 Thr Ser Val Leu Glu Met Val Arg Ala Phe Glu Met Ala Ser Gly Lys
 275 280 285
 Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Ile
 290 295 300
 Val Tyr Ala Ser Thr Lys Lys Ala Glu Arg Glu Leu Lys Trp Lys Ala
 305 310 315 320

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Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
325 330 335

Lys Asn Pro Tyr Gly Tyr Gly Asp Gln Gly Ser Thr Asp
340 345

<210> 23
<211> 490
<212> DNA
<213> *Triticum aestivum*

<220>
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<220>
<221> unsure
<222> (73)

<220>
<221> unsure
<222> (81)

<220>
<221> unsure
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<221> unsure
<222> (480)

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<221> unsure
<222> (482)

<400> 23
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ttccgcgtcc tcgtatcgac cagcctcgac aacgcctccg aggaggccat ccgcgcgtc 180
cgacaactcg ccaacgcccc gcaaaanagc ctcgacttcc gcaaggtgga cttcgtgac 240
aaggangcgc tcgaccaat ctttcctcc caaaggatac ttcnactttt ttccgcaaaa 300
aagaagtatc tttttcng cttattatta anaattaact atagtatatt attgagtcca 360
caaattaaat gttgattnt ccgtccgtcc cggccgtcgt gccagccanc canccgtntc 420
tgctgtata gcaaatacga ctcccttcta tcagnatcgt ngtcgtngt aggtgtcaan 480
cncctacgag 490

<210> 24
<211> 103
<212> PRT
<213> *Triticum aestivum*

<220>
<221> UNSURE
<222> (4)

<220>
<221> UNSURE
<222> (6)

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<220>
<221> UNSURE
<222> (61)

<220>
<221> UNSURE
<222> (74)

<220>
<221> UNSURE
<222> (86)

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<220>
 <221> UNSURE
 <222> (90)

<400> 24
 Thr Gly Gly Xaa Gly Xaa Ile Gly Ser His Thr Val Leu Gln Leu Leu
 1 5 10 15
 Leu Gln Gly Phe Arg Val Leu Val Val Asp Ser Leu Asp Asn Ala Ser
 20 25 30
 Glu Glu Ala Ile Arg Arg Val Arg Gln Leu Ala Asn Ala Pro Gln Xaa
 35 40 45
 Ser Leu Asp Phe Arg Lys Val Asp Leu Arg Asp Lys Xaa Ala Leu Asp
 50 55 60
 Gln Ile Phe Ser Ser Gln Arg Tyr Leu Xaa Leu Phe Ser Ala Lys Lys
 65 70 75 80
 Lys Tyr Leu Phe Ser Xaa Leu Leu Leu Xaa Ile Asn Tyr Ser Ile Leu
 85 90 95
 Leu Ser Pro Gln Ile Lys Cys
 100

<210> 25
 <211> 350
 <212> PRT
 <213> Pisum sativum

<400> 25
 Met Val Ala Ser Ser Gln Lys Ile Leu Val Thr Gly Ser Ala Gly Phe
 1 5 10 15
 Ile Gly Thr His Thr Val Val Gln Leu Leu Asn Asn Gly Phe Asn Val
 20 25 30
 Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Val Glu Arg
 35 40 45
 Val Arg Glu Val Val Gly Ser Asn Leu Ser Gln Asn Leu Glu Phe Thr
 50 55 60
 Leu Gly Asp Leu Arg Asn Lys Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80
 Ser Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
 85 90 95
 Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val Gly
 100 105 110
 Thr Ile Asn Leu Tyr Glu Val Met Ala Lys His Asn Cys Lys Lys Met
 115 120 125
 Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile Pro
 130 135 140

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Cys Val Glu Asp Phe Lys Leu Gln Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160
 Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu Pro
 165 170 175
 Glu Trp Arg Ile Val Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190
 Glu Ser Gly Lys Leu Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu
 195 200 205
 Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn
 210 215 220
 Val Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Ser Ala Ile Arg Asp
 225 230 235 240
 Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255
 Lys Leu Phe Thr Ser Glu Asn Ile Gly Cys Thr Ala Tyr Asn Leu Gly
 260 265 270
 Thr Gly Arg Gly Ser Ser Val Leu Glu Met Val Ala Ala Phe Glu Lys
 275 280 285
 Ala Ser Gly Lys Lys Ile Ala Leu Lys Leu Cys Pro Arg Arg Pro Gly
 290 295 300
 Asp Ala Thr Glu Val Tyr Ala Ser Thr Ala Lys Ala Glu Lys Glu Leu
 305 310 315 320
 Gly Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Gln Trp
 325 330 335
 Asn Trp Ala Lys Asn Asn Pro Trp Gly Tyr Ser Gly Lys Pro
 340 345 350
 <210> 26
 <211> 350
 <212> PRT
 <213> Cyamopsis tetragonoloba
 <400> 26
 Met Ser Ser Gln Thr Val Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
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 Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Lys Ala Val Val
 20 25 30
 Val Asp Asn Leu Asp Asn Ser Ser Glu Thr Ala Ile His Arg Val Lys
 35 40 45
 Glu Leu Ala Gly Lys Phe Ala Gly Asn Leu Ser Phe His Lys Leu Asp
 50 55 60
 Leu Arg Asp Arg Asp Ala Leu Glu Lys Ile Phe Ser Ser Thr Lys Phe
 65 70 75 80

Asp Ser Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
 85 90 95

 Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly Thr Ile Val
 100 105 110

 Leu Phe Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
 115 120 125

 Ser Ser Ala Thr Val Tyr Gly Leu Pro Lys Glu Val Pro Cys Thr Glu
 130 135 140

 Glu Phe Pro Leu Ser Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 145 150 155 160

 Ile Glu Glu Ile Cys Arg Asp Ile Tyr Arg Ala Glu Gln Glu Trp Lys
 165 170 175

 Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
 180 185 190

 Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
 195 200 205

 Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
 210 215 220

 Asn Asp Tyr Thr Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
 225 230 235 240

 Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg Lys Leu Asn
 245 250 255

 Asp Pro Lys Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
 260 265 270

 Thr Ser Val Leu Glu Met Val Lys Ala Phe Glu Gln Ala Ser Gly Lys
 275 280 285

 Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Val
 290 295 300

 Val Tyr Ala Ser Thr Asn Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala
 305 310 315 320

 Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
 325 330 335

 Lys Asn Pro Tyr Gly Tyr Gly Ser Glu Asp Ser Ser Asn
 340 345 350

 <210> 27
 <211> 13
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: oligonucleotide

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<400> 27 13
catggaggag cag

<210> 28
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